**Supplementary Figure 1.** Pre-built best practice pipelines and the third party software tools supported by Omics Pipe. Users can easily create custom pipelines from the existing modules and they can create new modules supporting additional third party software tools.
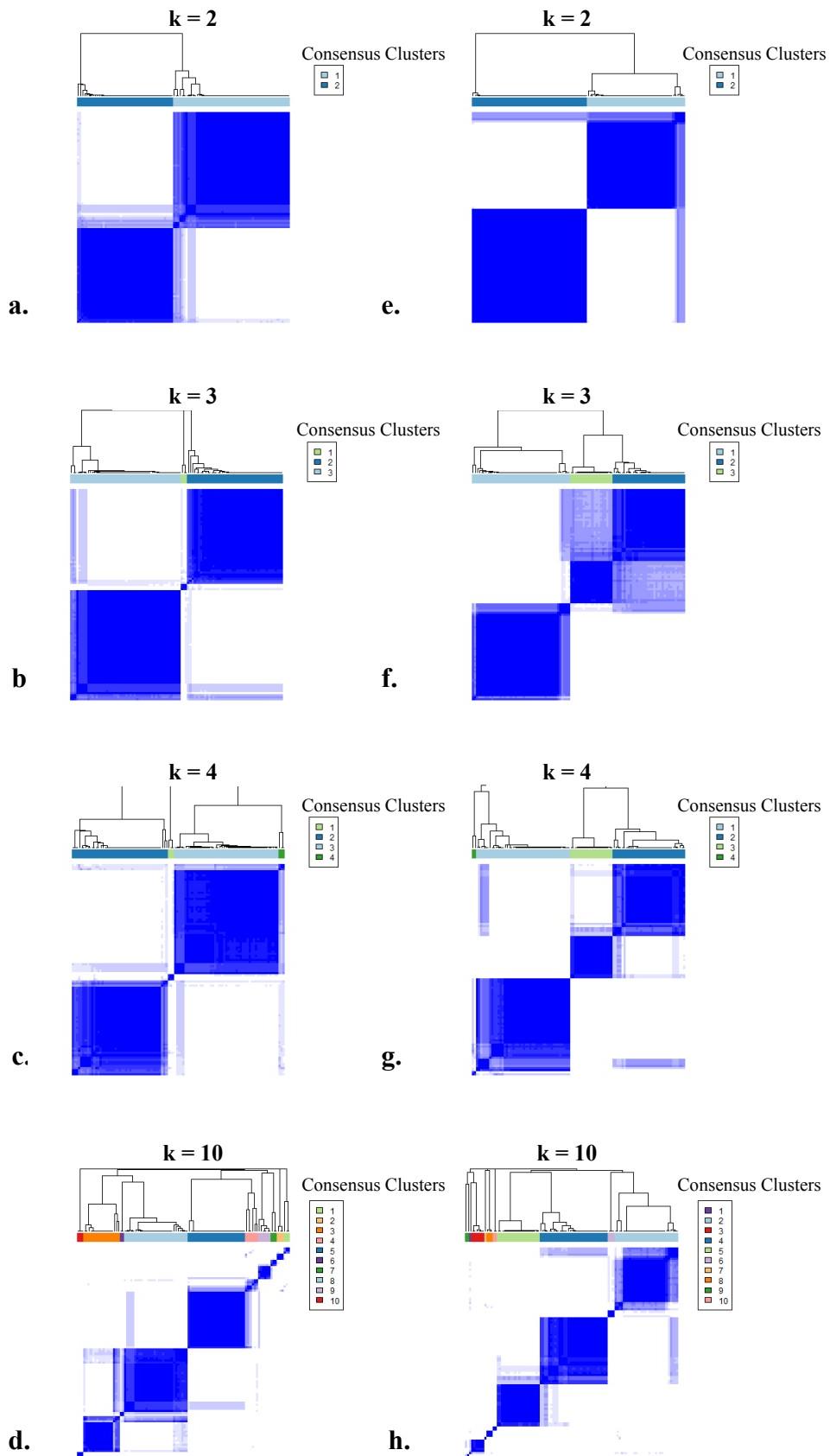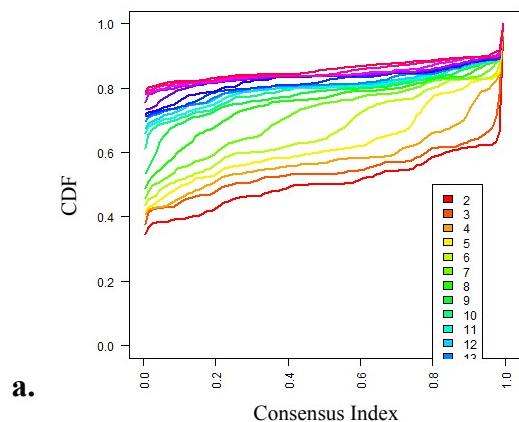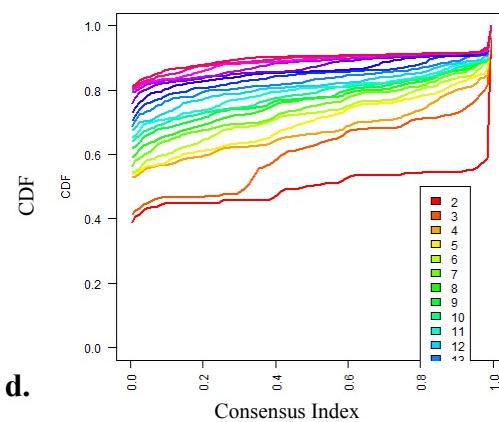
Supplementary Figure 2. Consensus clustering analysis of the TCGA breast invasive carcinoma paired tumor-normal samples performed with the reanalyzed count data (a)-(d) and the original raw counts downloaded from TCGA (e)-(h) for cluster sizes of k=2, k=3, k=4 and k=10. The blue and white heat map displays sample consensus.
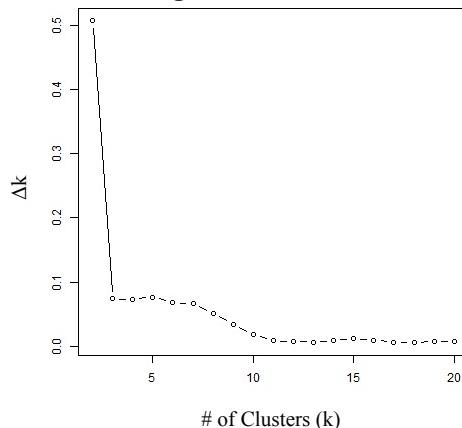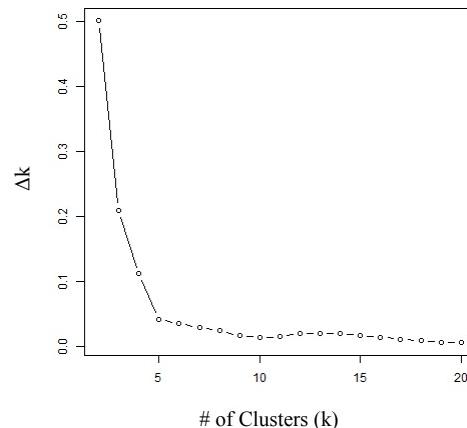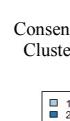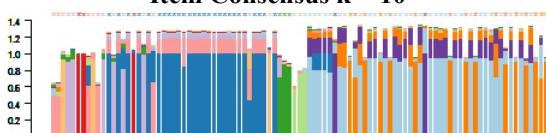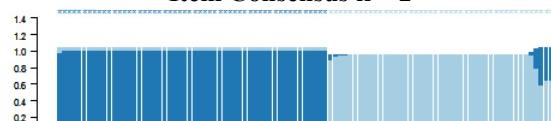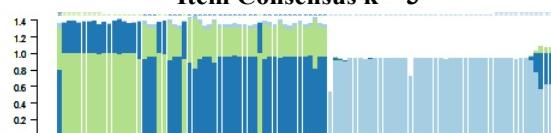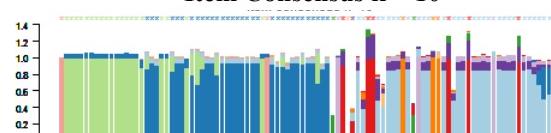
Supplementary Figure 3. Measurements of consensus for different cluster sizes (k) from the consensus clustering analysis on the reanalyzed (a)-(c) and original counts (d)-(f) from the TCGA paired tumor-normal breast invasive carcinoma samples. The empirical cumulative distribution (CDF) plots (a) and (d) indicate at which k the shape of the curve approaches the ideal step function. Plots (b) and (e) depict the area under the two CDF curves. Item consensus plots (c) and (f) demonstrate the mean consensus of each sample with all other samples in a particular cluster (represented by color).